



PTO/PCT Rec'd

14 AUG 2002

HS

SEQUENCE LISTING

<110> Northwest Biotherapeutics, Inc.

<120> METHODS FOR THE DIAGNOSIS AND TREATMENT OF METASTATIC
PROSTATE TUMORS

<130> 8511-025-228

<140> PCT/US99/08079

<141> 1999-04-13

<160> 16

<170> PatentIn Ver. 2.0

<210> 1

<211> 4450

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22) .. (3915)

<400> 1

acccacgcgc agcggccgga g	atg cag cgg ggc gcc gcg ctg tgc ctg cga	51
	Met Gln Arg Gly Ala Ala Leu Cys Leu Arg	
	1 5 10	
ctg tgg ctc tgc ctg gga ctc ctg gac ggc ctg gtg agt gac tac tcc	99	
Leu Trp Leu Cys Leu Gly Leu Leu Asp Gly Leu Val Ser Asp Tyr Ser		
	15 20 25	
atg acc ccc ccg acc ttg aac atc acg gag gag tca cac gtc atc gac	147	
Met Thr Pro Pro Thr Leu Asn Ile Thr Glu Glu Ser His Val Ile Asp		
	30 35 40	
acc ggt gac agc ctg tcc atc tcc tgc agg gga cag cac ccc ctc gag	195	
Thr Gly Asp Ser Leu Ser Ile Ser Cys Arg Gly Gln His Pro Leu Glu		
	45 50 55	
tgg gct tgg cca gga gct cag gag gcg cca gcc acc gga gac aag gac	243	
Trp Ala Trp Pro Gly Ala Gln Glu Ala Pro Ala Thr Gly Asp Lys Asp		
	60 65 70	
agc gag gac acg ggg gtg gtg cga gac tgc gag ggc aca gac gcc agg	291	
Ser Glu Asp Thr Gly Val Val Arg Asp Cys Glu Gly Thr Asp Ala Arg		
	75 80 85 90	
ccc tac tgc aag gtg ttg ctg ctg cac gag gta cat gcc aac gac aca	339	
Pro Tyr Cys Lys Val Leu Leu Leu His Glu Val His Ala Asn Asp Thr		
	95 100 105	
ggc agc tac gtc tgc tac tac aag tac atc aag gca cgc atc gag ggc	387	
Gly Ser Tyr Val Cys Tyr Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly		
	110 115 120	

acc acg gcc gcc agc tcc tac gtg ttc gtg aga gac ttt gag cag cca	435
Thr Thr Ala Ala Ser Ser Tyr Val Phe Val Arg Asp Phe Glu Gln Pro	
125 130 135	
ttc atc aac aag cct gac acg ctc ttg gtc aac agg aag gac gcc atg	483
Phe Ile Asn Lys Pro Asp Thr Leu Leu Val Asn Arg Lys Asp Ala Met	
140 145 150	
tgg gtg ccc tgt ctg gtg tcc atc ccc ggc ctc aat gtc acg ctg cgc	531
Trp Val Pro Cys Leu Val Ser Ile Pro Gly Leu Asn Val Thr Leu Arg	
155 160 165 170	
tcg caa agc tcg gtg ctg tgg cca gac ggg cag gag gtg gtg tgg gat	579
Ser Gln Ser Ser Val Leu Trp Pro Asp Gly Gln Glu Val Val Trp Asp	
175 180 185	
gac cgg cgg ggc atg ctc gtg tcc acg cca ctg ctg cac gat gcc ctg	627
Asp Arg Arg Gly Met Leu Val Ser Thr Pro Leu Leu His Asp Ala Leu	
190 195 200	
tac ctg cag tgc gag acc acc tgg gga gac cag gac ttc ctt tcc aac	675
Tyr Leu Gln Cys Glu Thr Thr Trp Gly Asp Gln Asp Phe Leu Ser Asn	
205 210 215	
ccc ttc ctg gtg cac atc aca ggc aac gag ctc tat gac atc cag ctg	723
Pro Phe Leu Val His Ile Thr Gly Asn Glu Leu Tyr Asp Ile Gln Leu	
220 225 230	
ttg ccc agg aag tcg ctg gag ctg ctg gta ggg gag aag ctg gtc ctc	771
Leu Pro Arg Lys Ser Leu Glu Leu Leu Val Gly Glu Lys Leu Val Leu	
235 240 245 250	
aac tgc acc gtg tgg gct gag ttt aac tca ggt gtc acc ttt gac tgg	819
Asn Cys Thr Val Trp Ala Glu Phe Asn Ser Gly Val Thr Phe Asp Trp	
255 260 265	
gac tac cca ggg aag cag gca gag cgg ggt aag tgg gtg ccc gag cga	867
Asp Tyr Pro Gly Lys Gln Ala Glu Arg Gly Lys Trp Val Pro Glu Arg	
270 275 280	
cgc tcc caa cag acc cac aca gaa ctc tcc agc atc ctg acc atc cac	915
Arg Ser Gln Gln Thr His Thr Glu Leu Ser Ser Ile Leu Thr Ile His	
285 290 295	
aac gtc agc cag cac gac ctg ggc tcg tat gtg tgc aag gcc aac aac	963
Asn Val Ser Gln His Asp Leu Gly Ser Tyr Val Cys Lys Ala Asn Asn	
300 305 310	
ggc atc cag cga ttt cgg gag agc acc gag gtc att gtg cat gaa aat	1011
Gly Ile Gln Arg Phe Arg Glu Ser Thr Glu Val Ile Val His Glu Asn	
315 320 325 330	
ccc ttc atc agc gtc gag tgg ctc aaa gga ccc atc ctg gag gcc acg	1059
Pro Phe Ile Ser Val Glu Trp Leu Lys Gly Pro Ile Leu Glu Ala Thr	
335 340 345	

gca gga gac gag ctg gtg aag ctg ccc gtg aag ctg gca gcg tac ccc Ala Gly Asp Glu Leu Val Lys Leu Pro Val Lys Leu Ala Ala Tyr Pro 350 355 360	1107
ccg ccc gag ttc cag tgg tac aag gat gga aag gca ctg tcc ggg cgc Pro Pro Glu Phe Gln Trp Tyr Lys Asp Gly Lys Ala Leu Ser Gly Arg 365 370 375	1155
cac agt cca cat gcc ctg gtg ctc aag gag gtg aca gag gcc agc aca His Ser Pro His Ala Leu Val Leu Lys Glu Val Thr Thr Glu Ala Ser Thr 380 385 390	1203
ggc acc tac acc ctc gcc ctg tgg aac tcc gct gct ggc ctg agg cgc Gly Thr Tyr Thr Leu Ala Leu Trp Asn Ser Ala Ala Gly Leu Arg Arg 395 400 405 410	1251
aac atc agc ctg gag ctg gtg gtg aat gtg ccc ccc cag ata cat gag Asn Ile Ser Leu Glu Leu Val Val Asn Val Pro Pro Gln Ile His Glu 415 420 425	1299
aag gag gcc tcc tcc ccc agc atc tac tcg cgt cac agc cgc cag gcc Lys Glu Ala Ser Ser Pro Ser Ile Tyr Ser Arg His Ser Arg Gln Ala 430 435 440	1347
ctc acc tgc acg gcc tac ggg gtg ccc ctg cct ctc agc atc cag tgg Leu Thr Cys Thr Ala Tyr Gly Val Pro Leu Pro Leu Ser Ile Gln Trp 445 450 455	1395
cac tgg cgg ccc tgg aca ccc tgc aag atg ttt gcc cag cgt agt ctc His Trp Arg Pro Trp Thr Pro Cys Lys Met Phe Ala Gln Arg Ser Leu 460 465 470	1443
cgg cgg cgg cag cag caa gac ctc atg cca cag tgc cgt gac tgg agg Arg Arg Arg Gln Gln Gln Asp Leu Met Pro Gln Cys Arg Asp Trp Arg 475 480 485 490	1491
gcg gtg acc acg cag gat gcc gtg aac ccc atc gag agc ctg gac acc Ala Val Thr Thr Gln Asp Ala Val Asn Pro Ile Glu Ser Leu Asp Thr 495 500 505	1539
tgg acc gag ttt gtg gag gga aag aat aag act gtg agc aag ctg gtg Trp Thr Glu Phe Val Glu Gly Lys Asn Lys Thr Val Ser Lys Leu Val 510 515 520	1587
atc cag aat gcc aac gtg tct gcc atg tac aag tgt gtg gtc tcc aac Ile Gln Asn Ala Asn Val Ser Ala Met Tyr Lys Cys Val Val Ser Asn 525 530 535	1635
aag gtg ggc cag gat gag cgg ctc atc tac ttc tat gtg acc acc atc Lys Val Gly Gln Asp Glu Arg Leu Ile Tyr Phe Tyr Val Thr Thr Ile 540 545 550	1683
ccc gac ggc ttc acc atc gaa tcc aag cca tcc gag gag cta cta gag Pro Asp Gly Phe Thr Ile Glu Ser Lys Pro Ser Glu Glu Leu Leu Glu 555 560 565 570	1731
ggc cag ccg gtg ctc ctg agc tgc caa gcc gac agc tac aag tac gag	1779

Gly	Gln	Pro	Val	Leu	Leu	Ser	Cys	Gln	Ala	Asp	Ser	Tyr	Lys	Tyr	Glu		
				575					580						585		
cat	ctg	cgc	tgg	tac	cgc	ctc	aac	ctg	tcc	acg	ctg	cac	gat	gcg	cac	1827	
His	Leu	Arg	Trp	Tyr	Arg	Leu	Asn	Leu	Ser	Thr	Leu	His	Asp	Ala	His		
			590					595					600				
ggg	aac	ccg	ctt	ctg	ctc	gac	tgc	aag	aac	gtg	cat	ctg	ttc	gcc	acc	1875	
Gly	Asn	Pro	Leu	Leu	Leu	Asp	Cys	Lys	Asn	Val	His	Leu	Phe	Ala	Thr		
		605					610					615					
cct	ctg	gcc	gcc	agc	ctg	gag	gag	gtg	gca	cct	ggg	gcg	cgc	cac	gcc	1923	
Pro	Leu	Ala	Ala	Ser	Leu	Glu	Glu	Val	Ala	Pro	Gly	Ala	Arg	His	Ala		
	620					625					630						
acg	ctc	agc	ctg	agt	atc	ccc	cgc	gtc	gcg	ccc	gag	cac	gag	ggc	cac	1971	
Thr	Leu	Ser	Leu	Ser	Ile	Pro	Arg	Val	Ala	Pro	Glu	His	Glu	Gly	His		
	635				640					645					650		
tat	gtg	tgc	gaa	gtg	caa	gac	cgg	cgc	agc	cat	gac	aag	cac	tgc	cac	2019	
Tyr	Val	Cys	Glu	Val	Gln	Asp	Arg	Arg	Ser	His	Asp	Lys	His	Cys	His		
				655					660					665			
aag	aag	tac	ctg	tcg	gtg	cag	gcc	ctg	gaa	gcc	cct	cgg	ctc	acg	cag	2067	
Lys	Lys	Tyr	Leu	Ser	Val	Gln	Ala	Leu	Glu	Ala	Pro	Arg	Leu	Thr	Gln		
			670					675					680				
aac	ttg	acc	gac	ctc	ctg	gtg	aac	gtg	agc	gac	tcg	ctg	gag	atg	cag	2115	
Asn	Leu	Thr	Asp	Leu	Leu	Val	Asn	Val	Ser	Asp	Ser	Leu	Glu	Met	Gln		
		685					690					695					
tgc	ttg	gtg	gcc	gga	gcg	cac	gcg	ccc	agc	atc	gtg	tgg	tac	aaa	gac	2163	
Cys	Leu	Val	Ala	Gly	Ala	His	Ala	Pro	Ser	Ile	Val	Trp	Tyr	Lys	Asp		
	700					705					710						
gag	agg	ctg	ctg	gag	gaa	aag	tct	gga	gtc	gac	ttg	gcg	gac	tcc	aac	2211	
Glu	Arg	Leu	Leu	Glu	Glu	Lys	Ser	Gly	Val	Asp	Leu	Ala	Asp	Ser	Asn		
	715				720					725					730		
cag	aag	ctg	agc	atc	cag	cgc	gtg	cgc	gag	gag	gat	gcg	gga	ccg	tat	2259	
Gln	Lys	Leu	Ser	Ile	Gln	Arg	Val	Arg	Glu	Glu	Asp	Ala	Gly	Pro	Tyr		
				735					740					745			
ctg	tgc	agc	gtg	tgc	aga	ccc	aag	ggc	tgc	gtc	aac	tcc	tcc	gcc	agc	2307	
Leu	Cys	Ser	Val	Cys	Arg	Pro	Lys	Gly	Cys	Val	Asn	Ser	Ser	Ala	Ser		
			750					755					760				
gtg	gcc	gtg	gaa	ggc	tcc	gag	gat	aag	ggc	agc	atg	gag	atc	gtg	atc	2355	
Val	Ala	Val	Glu	Gly	Ser	Glu	Asp	Lys	Gly	Ser	Met	Glu	Ile	Val	Ile		
		765					770					775					
ctt	gtc	ggt	acc	ggc	gtc	atc	gct	gtc	ttc	ttc	tgg	gtc	ctc	ctc	ctc	2403	
Leu	Val	Gly	Thr	Gly	Val	Ile	Ala	Val	Phe	Phe	Trp	Val	Leu	Leu	Leu		
	780					785					790						
ctc	atc	ttc	tgt	aac	atg	agg	agg	ccg	gcc	cac	gca	gac	atc	aag	acg	2451	
Leu	Ile	Phe	Cys	Asn	Met	Arg	Arg	Pro	Ala	His	Ala	Asp	Ile	Lys	Thr		

795		800		805		810	
ggc tac ctg tcc atc atc atg gac ccc ggg gag gtg cct ctg gag gag	2499						
Gly Tyr Leu Ser Ile Ile Met Asp Pro Gly Glu Val Pro Leu Glu Glu							
		815		820		825	
caa tgc gaa tac ctg tcc tac gat gcc agc cag tgg gaa ttc ccc cga	2547						
Gln Cys Glu Tyr Leu Ser Tyr Asp Ala Ser Gln Trp Glu Phe Pro Arg							
		830		835		840	
gag cgg ctg cac ctg ggg aga gtg ctc ggc tac ggc gcc ttc ggg aag	2595						
Glu Arg Leu His Leu Gly Arg Val Leu Gly Tyr Gly Ala Phe Gly Lys							
		845		850		855	
gtg gtg gaa gcc tcc gct ttc ggc atc cac aag ggc agc agc tgt gac	2643						
Val Val Glu Ala Ser Ala Phe Gly Ile His Lys Gly Ser Ser Cys Asp							
		860		865		870	
acc gtg gcc gtg aaa atg ctg aaa gag ggc gcc acg gcc agc gag cag	2691						
Thr Val Ala Val Lys Met Leu Lys Glu Gly Ala Thr Ala Ser Glu Gln							
		875		880		885	890
cgc gcg ctg atg tcg gag ctc aag atc ctc att cac atc ggc aac cac	2739						
Arg Ala Leu Met Ser Glu Leu Lys Ile Leu Ile His Ile Gly Asn His							
		895		900		905	
ctc aac gtg gtc aac ctc ctc ggg gcg tgc acc aag ccg cag ggc ccc	2787						
Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr Lys Pro Gln Gly Pro							
		910		915		920	
ctc atg gtg atc gtg gag ttc tgc aag tac ggc aac ctc tcc aac ttc	2835						
Leu Met Val Ile Val Glu Phe Cys Lys Tyr Gly Asn Leu Ser Asn Phe							
		925		930		935	
ctg cgc gcc aag cgg gac gcc ttc agc ccc tgc gcg gag aag tct ccc	2883						
Leu Arg Ala Lys Arg Asp Ala Phe Ser Pro Cys Ala Glu Lys Ser Pro							
		940		945		950	
gag cag cgc gga cgc ttc cgc gcc atg gtg gag ctc gcc agg ctg gat	2931						
Glu Gln Arg Gly Arg Phe Arg Ala Met Val Glu Leu Ala Arg Leu Asp							
		955		960		965	970
cgg agg cgg ccg ggg agc agc gac agg gtc ctc ttc gcg cgg ttc tcg	2979						
Arg Arg Arg Pro Gly Ser Ser Asp Arg Val Leu Phe Ala Arg Phe Ser							
		975		980		985	
aag acc gag ggc gga gcg agg cgg gct tct cca gac caa gaa gct gag	3027						
Lys Thr Glu Gly Gly Ala Arg Arg Ala Ser Pro Asp Gln Glu Ala Glu							
		990		995		1000	
gac ctg tgg ctg agc ccg ctg acc atg gaa gat ctt gtc tgc tac agc	3075						
Asp Leu Trp Leu Ser Pro Leu Thr Met Glu Asp Leu Val Cys Tyr Ser							
		1005		1010		1015	
ttc cag gtg gcc aga ggg atg gag ttc ctg gct tcc cga aag tgc atc	3123						
Phe Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Arg Lys Cys Ile							
		1020		1025		1030	

cac aga gac ctg gct gct cgg aac att ctg ctg tcg gaa agc gac gtg His Arg Asp Leu Ala Ala Arg Asn Ile Leu Leu Ser Glu Ser Asp Val 1035 1040 1045 1050	3171
gtg aag atc tgt gac ttt ggc ctt gcc cgg gac atc tac aaa gac ccc Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro 1055 1060 1065	3219
gac tac gtc cgc aag ggc agt gcc cgg ctg ccc ctg aag tgg atg gcc Asp Tyr Val Arg Lys Gly Ser Ala Arg Leu Pro Leu Lys Trp Met Ala 1070 1075 1080	3267
cct gaa agc atc ttc gac aag gtg tac acc acg cag agt gac gtg tgg Pro Glu Ser Ile Phe Asp Lys Val Tyr Thr Thr Gln Ser Asp Val Trp 1085 1090 1095	3315
tcc ttt ggg gtg ctt ctc tgg gag atc ttc tct ctg ggg gcc tcc ccg Ser Phe Gly Val Leu Leu Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro 1100 1105 1110	3363
tac cct ggg gtg cag atc aat gag gag ttc tgc cag cgc gtg aga gac Tyr Pro Gly Val Gln Ile Asn Glu Glu Phe Cys Gln Arg Val Arg Asp 1115 1120 1125 1130	3411
ggc aca agg atg agg gcc ccg gag ctg gcc act ccc gcc ata cgc cac Gly Thr Arg Met Arg Ala Pro Glu Leu Ala Thr Pro Ala Ile Arg His 1135 1140 1145	3459
atc atg ctg aac tgc tgg tcc gga gac ccc aag gcg aga cct gca ttc Ile Met Leu Asn Cys Trp Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe 1150 1155 1160	3507
tcg gac ctg gtg gag atc ctg ggg gac ctg ctc cag ggc agg ggc ctg Ser Asp Leu Val Glu Ile Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu 1165 1170 1175	3555
caa gag gaa gag gag gtc tgc atg gcc ccg cgc agc tct cag agc tca Gln Glu Glu Glu Glu Val Cys Met Ala Pro Arg Ser Ser Gln Ser Ser 1180 1185 1190	3603
gaa gag ggc agc ttc tcg cag gtg tcc acc atg gcc cta cac atc gcc Glu Glu Gly Ser Phe Ser Gln Val Ser Thr Met Ala Leu His Ile Ala 1195 1200 1205 1210	3651
cag gct gac gct gag gac agc ccg cca agc ctg cag cgc cac agc ctg Gln Ala Asp Ala Glu Asp Ser Pro Pro Ser Leu Gln Arg His Ser Leu 1215 1220 1225	3699
gcc gcc agg tat tac aac tgg gtg tcc ttt ccc ggg tgc ctg gcc aga Ala Ala Arg Tyr Tyr Asn Trp Val Ser Phe Pro Gly Cys Leu Ala Arg 1230 1235 1240	3747
ggg gct gag acc cgt ggt tcc tcc agg atg aag aca ttt gag gaa ttc Gly Ala Glu Thr Arg Gly Ser Ser Arg Met Lys Thr Phe Glu Glu Phe 1245 1250 1255	3795

ccc atg acc cca acg acc tac aaa ggc tct gtg gac aac cag aca gac 3843
 Pro Met Thr Pro Thr Thr Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp
 1260 1265 1270

agt ggg atg gtg ctg gcc tcg gag gag ttt gag cag ata gag agc agg 3891
 Ser Gly Met Val Leu Ala Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg
 1275 1280 1285 1290

cat aga caa gaa agc ggc ttc agg tagctgaagc agagagagag aaggcagcat 3945
 His Arg Gln Glu Ser Gly Phe Arg
 1295

acgtcagcat tttcttctct gcacttataa gaaagatcaa agactttaag actttcgcta 4005
 tttcttctac tgctatctac tacaaacttc aaagaggaac caggaggaca agaggagcat 4065
 gaaagtggac aaggagtgtg accactgaag caccacaggg aggggttagg cctccggatg 4125
 actgcgggca ggccctggata atatccagcc tcccacaaga agctggtgga gcagagtgtt 4185
 ccctgactcc tccaaggaaa gggagacgcc ctttcatggt ctgctgagta acaggtgcct 4245
 tcccagacac tggcgttact gcttgaccaa agagccctca agcggccctt atgccagcgt 4305
 gacagagggc tcacctcttg ctttctaggt cacttctcac aatgtccctt cagcacctga 4365
 ccctgtgccc gccgattatt ccttggtaat atgagtaata catcaaagag tagtattaaa 4425
 agctaattaa tcatgtttat aaaaa 4450

<210> 2

<211> 1298

<212> PRT

<213> Homo sapiens

<400> 2

Met Gln Arg Gly Ala Ala Leu Cys Leu Arg Leu Trp Leu Cys Leu Gly
 1 5 10 15

Leu Leu Asp Gly Leu Val Ser Asp Tyr Ser Met Thr Pro Pro Thr Leu
 20 25 30

Asn Ile Thr Glu Glu Ser His Val Ile Asp Thr Gly Asp Ser Leu Ser
 35 40 45

Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Ala Trp Pro Gly Ala
 50 55 60

Gln Glu Ala Pro Ala Thr Gly Asp Lys Asp Ser Glu Asp Thr Gly Val
 65 70 75 80

Val Arg Asp Cys Glu Gly Thr Asp Ala Arg Pro Tyr Cys Lys Val Leu
 85 90 95

Leu Leu His Glu Val His Ala Asn Asp Thr Gly Ser Tyr Val Cys Tyr
 100 105 110

Tyr	Lys	Tyr	Ile	Lys	Ala	Arg	Ile	Glu	Gly	Thr	Thr	Ala	Ala	Ser	Ser		
	115						120					125					
Tyr	Val	Phe	Val	Arg	Asp	Phe	Glu	Gln	Pro	Phe	Ile	Asn	Lys	Pro	Asp		
	130					135					140						
Thr	Leu	Leu	Val	Asn	Arg	Lys	Asp	Ala	Met	Trp	Val	Pro	Cys	Leu	Val		
145					150					155					160		
Ser	Ile	Pro	Gly	Leu	Asn	Val	Thr	Leu	Arg	Ser	Gln	Ser	Ser	Val	Leu		
			165						170					175			
Trp	Pro	Asp	Gly	Gln	Glu	Val	Val	Trp	Asp	Asp	Arg	Arg	Gly	Met	Leu		
			180					185					190				
Val	Ser	Thr	Pro	Leu	Leu	His	Asp	Ala	Leu	Tyr	Leu	Gln	Cys	Glu	Thr		
	195						200					205					
Thr	Trp	Gly	Asp	Gln	Asp	Phe	Leu	Ser	Asn	Pro	Phe	Leu	Val	His	Ile		
	210					215					220						
Thr	Gly	Asn	Glu	Leu	Tyr	Asp	Ile	Gln	Leu	Leu	Pro	Arg	Lys	Ser	Leu		
225					230				235						240		
Glu	Leu	Leu	Val	Gly	Glu	Lys	Leu	Val	Leu	Asn	Cys	Thr	Val	Trp	Ala		
				245					250				255				
Glu	Phe	Asn	Ser	Gly	Val	Thr	Phe	Asp	Trp	Asp	Tyr	Pro	Gly	Lys	Gln		
		260						265					270				
Ala	Glu	Arg	Gly	Lys	Trp	Val	Pro	Glu	Arg	Arg	Ser	Gln	Gln	Thr	His		
	275						280					285					
Thr	Glu	Leu	Ser	Ser	Ile	Leu	Thr	Ile	His	Asn	Val	Ser	Gln	His	Asp		
	290					295					300						
Leu	Gly	Ser	Tyr	Val	Cys	Lys	Ala	Asn	Asn	Gly	Ile	Gln	Arg	Phe	Arg		
305					310				315						320		
Glu	Ser	Thr	Glu	Val	Ile	Val	His	Glu	Asn	Pro	Phe	Ile	Ser	Val	Glu		
				325					330					335			
Trp	Leu	Lys	Gly	Pro	Ile	Leu	Glu	Ala	Thr	Ala	Gly	Asp	Glu	Leu	Val		
			340					345					350				
Lys	Leu	Pro	Val	Lys	Leu	Ala	Ala	Tyr	Pro	Pro	Pro	Glu	Phe	Gln	Trp		
	355						360					365					
Tyr	Lys	Asp	Gly	Lys	Ala	Leu	Ser	Gly	Arg	His	Ser	Pro	His	Ala	Leu		
	370					375					380						
Val	Leu	Lys	Glu	Val	Thr	Glu	Ala	Ser	Thr	Gly	Thr	Tyr	Thr	Leu	Ala		
385					390					395					400		
Leu	Trp	Asn	Ser	Ala	Ala	Gly	Leu	Arg	Arg	Asn	Ile	Ser	Leu	Glu	Leu		
				405					410					415			

Val	Val	Asn	Val	Pro	Pro	Gln	Ile	His	Glu	Lys	Glu	Ala	Ser	Ser	Pro	420	425	430
Ser	Ile	Tyr	Ser	Arg	His	Ser	Arg	Gln	Ala	Leu	Thr	Cys	Thr	Ala	Tyr	435	440	445
Gly	Val	Pro	Leu	Pro	Leu	Ser	Ile	Gln	Trp	His	Trp	Arg	Pro	Trp	Thr	450	455	460
Pro	Cys	Lys	Met	Phe	Ala	Gln	Arg	Ser	Leu	Arg	Arg	Arg	Gln	Gln	Gln	465	470	475
Asp	Leu	Met	Pro	Gln	Cys	Arg	Asp	Trp	Arg	Ala	Val	Thr	Thr	Gln	Asp	485	490	495
Ala	Val	Asn	Pro	Ile	Glu	Ser	Leu	Asp	Thr	Trp	Thr	Glu	Phe	Val	Glu	500	505	510
Gly	Lys	Asn	Lys	Thr	Val	Ser	Lys	Leu	Val	Ile	Gln	Asn	Ala	Asn	Val	515	520	525
Ser	Ala	Met	Tyr	Lys	Cys	Val	Val	Ser	Asn	Lys	Val	Gly	Gln	Asp	Glu	530	535	540
Arg	Leu	Ile	Tyr	Phe	Tyr	Val	Thr	Thr	Ile	Pro	Asp	Gly	Phe	Thr	Ile	545	550	555
Glu	Ser	Lys	Pro	Ser	Glu	Glu	Leu	Leu	Glu	Gly	Gln	Pro	Val	Leu	Leu	565	570	575
Ser	Cys	Gln	Ala	Asp	Ser	Tyr	Lys	Tyr	Glu	His	Leu	Arg	Trp	Tyr	Arg	580	585	590
Leu	Asn	Leu	Ser	Thr	Leu	His	Asp	Ala	His	Gly	Asn	Pro	Leu	Leu	Leu	595	600	605
Asp	Cys	Lys	Asn	Val	His	Leu	Phe	Ala	Thr	Pro	Leu	Ala	Ala	Ser	Leu	610	615	620
Glu	Glu	Val	Ala	Pro	Gly	Ala	Arg	His	Ala	Thr	Leu	Ser	Leu	Ser	Ile	625	630	635
Pro	Arg	Val	Ala	Pro	Glu	His	Glu	Gly	His	Tyr	Val	Cys	Glu	Val	Gln	645	650	655
Asp	Arg	Arg	Ser	His	Asp	Lys	His	Cys	His	Lys	Lys	Tyr	Leu	Ser	Val	660	665	670
Gln	Ala	Leu	Glu	Ala	Pro	Arg	Leu	Thr	Gln	Asn	Leu	Thr	Asp	Leu	Leu	675	680	685
Val	Asn	Val	Ser	Asp	Ser	Leu	Glu	Met	Gln	Cys	Leu	Val	Ala	Gly	Ala	690	695	700
His	Ala	Pro	Ser	Ile	Val	Trp	Tyr	Lys	Asp	Glu	Arg	Leu	Leu	Glu	Glu	705	710	715
																		720

Lys	Ser	Gly	Val	Asp	Leu	Ala	Asp	Ser	Asn	Gln	Lys	Leu	Ser	Ile	Gln	725	730	735
Arg	Val	Arg	Glu	Glu	Asp	Ala	Gly	Pro	Tyr	Leu	Cys	Ser	Val	Cys	Arg	740	745	750
Pro	Lys	Gly	Cys	Val	Asn	Ser	Ser	Ala	Ser	Val	Ala	Val	Glu	Gly	Ser	755	760	765
Glu	Asp	Lys	Gly	Ser	Met	Glu	Ile	Val	Ile	Leu	Val	Gly	Thr	Gly	Val	770	775	780
Ile	Ala	Val	Phe	Phe	Trp	Val	Leu	Leu	Leu	Leu	Ile	Phe	Cys	Asn	Met	785	790	795
Arg	Arg	Pro	Ala	His	Ala	Asp	Ile	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Ile	805	810	815
Met	Asp	Pro	Gly	Glu	Val	Pro	Leu	Glu	Glu	Gln	Cys	Glu	Tyr	Leu	Ser	820	825	830
Tyr	Asp	Ala	Ser	Gln	Trp	Glu	Phe	Pro	Arg	Glu	Arg	Leu	His	Leu	Gly	835	840	845
Arg	Val	Leu	Gly	Tyr	Gly	Ala	Phe	Gly	Lys	Val	Val	Glu	Ala	Ser	Ala	850	855	860
Phe	Gly	Ile	His	Lys	Gly	Ser	Ser	Cys	Asp	Thr	Val	Ala	Val	Lys	Met	865	870	875
Leu	Lys	Glu	Gly	Ala	Thr	Ala	Ser	Glu	Gln	Arg	Ala	Leu	Met	Ser	Glu	885	890	895
Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	Asn	His	Leu	Asn	Val	Val	Asn	Leu	900	905	910
Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gln	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	915	920	925
Phe	Cys	Lys	Tyr	Gly	Asn	Leu	Ser	Asn	Phe	Leu	Arg	Ala	Lys	Arg	Asp	930	935	940
Ala	Phe	Ser	Pro	Cys	Ala	Glu	Lys	Ser	Pro	Glu	Gln	Arg	Gly	Arg	Phe	945	950	955
Arg	Ala	Met	Val	Glu	Leu	Ala	Arg	Leu	Asp	Arg	Arg	Arg	Pro	Gly	Ser	965	970	975
Ser	Asp	Arg	Val	Leu	Phe	Ala	Arg	Phe	Ser	Lys	Thr	Glu	Gly	Gly	Ala	980	985	990
Arg	Arg	Ala	Ser	Pro	Asp	Gln	Glu	Ala	Glu	Asp	Leu	Trp	Leu	Ser	Pro	995	1000	1005
Leu	Thr	Met	Glu	Asp	Leu	Val	Cys	Tyr	Ser	Phe	Gln	Val	Ala	Arg	Gly	1010	1015	1020

Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala
 025 1030 1035 1040
 Arg Asn Ile Leu Leu Ser Glu Ser Asp Val Val Lys Ile Cys Asp Phe
 1045 1050 1055
 Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly
 1060 1065 1070
 Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp
 1075 1080 1085
 Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu
 1090 1095 1100
 Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile
 1105 1110 1115 1120
 Asn Glu Glu Phe Cys Gln Arg Val Arg Asp Gly Thr Arg Met Arg Ala
 1125 1130 1135
 Pro Glu Leu Ala Thr Pro Ala Ile Arg His Ile Met Leu Asn Cys Trp
 1140 1145 1150
 Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Asp Leu Val Glu Ile
 1155 1160 1165
 Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln Glu Glu Glu Val
 1170 1175 1180
 Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser
 1185 1190 1195 1200
 Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp
 1205 1210 1215
 Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn
 1220 1225 1230
 Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly
 1235 1240 1245
 Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr
 1250 1255 1260
 Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala
 1265 1270 1275 1280
 Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly
 1285 1290 1295
 Phe Arg

<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 3
ggcgccccgc tgcac

15

<210> 4
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 4
cgaagtgggtg aagttcatgg atg

23

<210> 5
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 5
ttctgtatca gtctttcctg gtgag

25

<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 6
ctggcatggc cttctgtgaa agca

24

<210> 7
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 7

aataccagtg gatgtgatgc gg

22

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 8

taccacagtg tcaggcagcg

20

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 9

atcaaattct cggttggccc

20

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 10

agagggatgg agttcctggc

20

<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

aataccagtg gatgtgatgc gg

22

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 12

agacagcaga aagttcatgg t

21

<210> 13

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 13

caagtgcattg gtgga

15

<210> 14

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 14

caccttgctc tgcatt

15

<210> 15

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 15

cccgggtgtcc caga

14

<210> 16

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 16

tacgtagtatt ggtgtac

17